Microbial Community Structure and its Relationship to Gut Health in Poultry

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Introduction

A condition known to commercial turkey producers in Minnesota as "Light Turkey Syndrome" or "LTS" has plagued the industry for several years. LTS refers to observations by Minnesota turkey producers that regional flocks are consistently below growth potential, and often display great bird-to-bird variability within a flock. Poults from the same supplier perform significantly better in farms outside of MN. This condition apparently occurs in the absence of detectable disease issues. Based on experimental data thus far, LTS is a multifactorial issue that does not likely involve a single pathogen. While it does not appear to cause outright increases in mortality, the economic impacts are huge. It is estimated by the MN turkey industry that annual losses in revenue due to LTS exceed $24.7 million and are significantly reducing the ability of MN turkey growers to be competitive in the national and international markets. Study of LTS in turkeys has been hampered by the lack of a refined case definition. The goal of this work was to better understand differences in the small intestinal microflora of birds belonging to flocks experiencing LTS versus those achieving expected market weights, and to correlate the small intestinal microflora with individual bird weight at different timepoints during the brood and growout periods.

Methods

Ileum samples were collected from several different flocks classified as "LTS" or "normal" over the course of twelve weeks. At selected timepoints, ten birds from each flock were randomly selected, euthanized, and their gut contents collected. Sequencing of the 16S rRNA V3 hypervariable region was performed to collect 10,000 sequences per bird analyzed. Weights, cecum scores, and intestinal lengths were also recorded. Sequences were analyzed to determine the relative proportions of bacterial species present in each bird at the selected timepoints.

Results

The predominant species present in the ileum belonged to the *Lactobacillus* genus. However, species-level analysis revealed that a predictable pattern could be observed in the succession of *Lactobacillus* species over time. Additionally, an unculturable organism known as Candidatus Arthromitus was present at significantly higher proportions in birds of normal weights at early timepoints. The presence of Candidatus Arthromitus was associated with acceleration in the colonization of *Lactobacillus* species associated with mature birds, such as *L. aviarius* and *L. johnsonii*. These results suggest that normal weight birds follow this typical succession of bacterial species, while this succession is delayed in LTS birds.

Conclusions

A predictable succession of bacterial species in the turkey ileum is associated with normal weight gain over time. This succession is delayed in birds and flocks experiencing LTS. We do not know at this time whether this relationship is direct or indirect, and follow-up inoculation studies are ongoing to determine the precise role of these bacteria in bird development and normal weight gain.

Notes